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To Whom It May Concern:

Ed Feigenbaum and Robert Inglemoor have discussed with me their plans for computer interpretation of vector (Patterson) maps which can be generated from x-ray crystallography intensity data.

Several groups have worked on vector search methods on small to moderate size structures. Early work was done by Hoppe (Elektrochem. 61, 1076 (1957), Sparks (ACA meeting Boulder, Colo.(1961)) and Nordman and Nakatsu (JACS 85, 353 (1963)). Probably the best programs are those of Braun, Hornstra and Leenhouts (Philips Res., Rep. 24, 85, 427 (1969)). Christensen, of our laboratories, has recently used these programs for solving the structure of Synalar.

To my knowledge, these methods have not been used to solve an unknown protein or polynucleotide structure although Love at Johns Hopkins University will soon attempt to solve sickle cell hemoglobin by this method (private communication). Nordman and Schilling (Crystallographic Computing, Munksgaard, Copenhagen P.110-114(1969)) have shown the power of this method by finding the heme group and a 4-turn α-helix in the myoglobin structure.

In my opinion, success with current programs is primarily dependent on the size and accuracy with which molecular fragments are known and on the amount of computer time which is available (searches for large numbers of vectors can be very time consuming).

Although I doubt whether this approach will lead to a general solution for macromolecules, I believe that Ed Feigenbaum and Robert Inglemoor's talents in Combinatorial Analysis could lead to significant advances concerning size and accuracy with which molecular fragments must be known and to improved algorithms which would be more efficient of computer time.

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RAS:jb

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